7,1330

<110> Botstein,David
Desnoyers,Luc
Ferrara,Napoleone
Fong,Sherman
Gao,Wei-Qiang
Goddard,Audrey
Gurney,Austin L.
Pan,James
Roy,Margaret Ann
Stewart,Timothy A.
Tumas,Daniel
Watanabe,Colin K.
Wood,William I.

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 cgggatgacc cgccgggacc cgctcgcaaa taaggtggcc ctggtaacgg 150

 cctccaccga cgggatcggc ttcgccatcg cccggcgttt ggcccaggac 200

 ggggcccatg tggtcgtcag cagccggaag cagcagaatg tggaccaggc 250

 ggtggccacg ctgcaggggg aggggctgag cgtgacgggc accgtgtgcc 300

 atgtggggaa ggcggaggac cgggagcggc tggtggccac ggctgtgaag .350

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acattaatgt gaaggcccca gccctgatga caaaggcagt ggtgccagaa 500

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agggtgaact gcctagcacc tggacttatc aagactagct tcagcaggat 700

gctctggatg gacaaggaaa aagaggaaag catgaaagaa accctgcgga 750

taagaaggtt aggcgagcca gaggattgtg ctggcatcgt gtctttcctg 800

tgctctgaag atgccagcta catcactggg gaaacagtgg tggtgggtgg 850

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ttgggctcta gctcctggtg ctgttcctgc attcacccac tggcctttcc 950

cacctctgct caccttactg ttcacctcat caaatcagtt ctgccctgtg 1000

aaaagatcca gccttccctg ccgtcaaggt ggcgtcttac tcgggattcc 1050

tgctgttgtt gtggccttgg gtaaaggcct cccctgagaa cacaggacag 1100

gcctgctgac aaggctgagt ctaccttggc aaagaccaag atatttttc 1150

ctgggccact ggtgaatctg aggggtgatg ggagagaagg aacctggagt 1200

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Ala Asn Lys Val Ala Leu Val Thr Ala Ser Thr Asp Gly Ile Gly
                35                  40                  45

Phe Ala Ile Ala Arg Arg Leu Ala Gln Asp Gly Ala His Val Val
                50                  55                  60

Val Ser Ser Arg Lys Gln Gln Asn Val Asp Gln Ala Val Ala Thr
                65                  70                  75
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3

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            80                    85                    90

Gly Lys Ala Glu Asp Arg Glu Arg Leu Val Ala Thr Ala Val Lys
            95                    100                  105

Leu His Gly Gly Ile Asp Ile Leu Val Ser Asn Ala Ala Val Asn
            110                   115                  120

Pro Phe Phe Gly Ser Ile Met Asp Val Thr Glu Glu Val Trp Asp
            125                   130                  135

Lys Thr Leu Asp Ile Asn Val Lys Ala Pro Ala Leu Met Thr Lys
            140                   145                  150

Ala Val Val Pro Glu Met Glu Lys Arg Gly Gly Gly Ser Val Val
            155                   160                  165

Ile Val Ser Ser Ile Ala Ala Phe Ser Pro Ser Pro Gly Phe Ser
            170                   175                  180

Pro Tyr Asn Val Ser Lys Thr Ala Leu Leu Gly Leu Thr Lys Thr
            185                   190                  195

Leu Ala Ile Glu Leu Ala Pro Arg Asn Ile Arg Val Asn Cys Leu
            200                   205                  210

Ala Pro Gly Leu Ile Lys Thr Ser Phe Ser Arg Met Leu Trp Met
            215                   220                  225

Asp Lys Glu Lys Glu Glu Ser Met Lys Glu Thr Leu Arg Ile Arg
            230                   235                  240

Arg Leu Gly Glu Pro Glu Asp Cys Ala Gly Ile Val Ser Phe Leu
            245                   250                  255

Cys Ser Glu Asp Ala Ser Tyr Ile Thr Gly Glu Thr Val Val Val
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Gly Gly Gly Thr Pro Ser Arg Leu
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<223> Synthetic Oligonucleotide Probe

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<210> 5
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<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 5
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<212> DNA
<213> Homo sapiens

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 agaaccgaga ctttctggct gcgctggagg acgccatgga gcagtacaaa 200

 ctgcagagcg accggctgcg tgagcagcag gaggagatgg tggaactgcg 250

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 atggcctgcc tcccgggtcc tttgtgcctc gacctcatac agcccccctg 350

 gggggtgccc acgcccatgt gctgggcatg gtgccgcctg cctgcctccc 400

 tggagatgaa gttggctctg agcagagggg agagcaggtg acaaatggca 450

 gggaggctgg agctgagttg ctgactgagg tgaacaggct gggaagtggc 500

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5

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gttccgcagg agggtcgctg cggcccagag ccaggtgcag gtgctgaagg 1050

agaagaagca ggctacggag cggctggtgt cactgtcggc ccagagtgag 1100

aagcgactgc aggagctcga gcggaacgtg cagctcatgc ggcagcagca 1150

gggacagctg cagaggcggc ttcgcgagga dacggagcag aagcggcgcc 1200

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aagcatgagc aacagcagaa gatcctgaag attaagacgg aagagatcgc 1300

ggccttccag aggaagaggc gcagtggcag caacggctct gtggtcagcc 1350

tggaacagca gcagaagatt gaggagcaga gaagtggct ggaccaggag 1400

atggagaagg tgctacagca gcggcgggcg ctggaggagc tgggggagga 1450

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gaggacatcg tgcgagtgtc cagccggctg gagcacctgg agaaggagct 1600

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ggccaagctc agctacctct catcctcaga gaccagagcc ctcctctgca 1950

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cagcagagtc gagaccacct cggtgaaggg ttagcagaca gcaggaggca 2200

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ggataaacca ggaactgaaa cagaagctcg gcggtgtgaa cgctgtaggc 2300

cacagcaggg gtggggagaa gaggagcctg tgctcggagg gcagacaggc 2350
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6

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gtccacgctc cgttaccctt gacctggaaa cgctcgagcc tgtgtggtga 2500

ggagcagggg tcccccgagg aactgaggca gcgggaggcg gctgagcccc 2550

tggtggggcg ggtgcttcct gtgggtgagg caggcctgcc ctggaacttt 2600

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gattgatgtc cggaaaaacc ccctgtaagc cctcggggca gaccctgcct 2700

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<211> 830
<212> PRT
<213> Homo sapiens

<400> 7

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            20              25                  30

Gly Trp Gly Gly Leu Arg Leu Leu Asn Gly Leu Pro Pro Gly Ser
            35                  40                  45

Phe Val Pro Arg Pro His Thr Ala Pro Leu Gly Gly Ala His Ala
            50                  55                  60

His Val Leu Gly Met Val Pro Pro Ala Cys Leu Pro Gly Asp Glu
            65                  70                  75

Val Gly Ser Glu Gln Arg Gly Glu Gln Val Thr Asn Gly Arg Glu
            80                  85                  90

Ala Gly Ala Glu Leu Leu Thr Glu Val Asn Arg Leu Gly Ser Gly
            95                  100                 105
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7

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Ser Ser Ala Ala Ser Glu Glu Glu Glu Glu Glu Glu Pro Pro
                110                 115                 120

Arg Arg Thr Leu His Leu Arg Arg Asn Arg Ile Ser Asn Cys Ser
                125                 130                 135

Gln Arg Ala Gly Ala Arg Pro Gly Ser Leu Pro Glu Arg Lys Gly
                140                 145                 150

Pro Glu Leu Cys Leu Glu Glu Leu Asp Ala Ala Ile Pro Gly Ser
                155                 160                 165

Arg Ala Val Gly Gly Ser Lys Ala Arg Val Gln Ala Arg Gln Val
                170                 175                 180

Pro Pro Ala Thr Ala Ser Glu Trp Arg Leu Ala Gln Ala Gln Gln
                185                 190                 195

Lys Ile Arg Glu Leu Ala Ile Asn Ile Arg Met Lys Glu Glu Leu
                200                 205                 210

Ile Gly Glu Leu Val Arg Thr Gly Lys Ala Ala Gln Ala Leu Asn
                215                 220                 225

Arg Gln His Ser Gln Arg Ile Arg Glu Leu Glu Gln Glu Ala Glu
                230                 235                 240

Gln Val Arg Ala Glu Leu Ser Glu Gly Gln Arg Gln Leu Arg Glu
                245                 250                 255

Leu Glu Gly Lys Glu Leu Gln Asp Ala Gly Glu Arg Ser Arg Leu
                260                 265                 270

Gln Glu Phe Arg Arg Arg Val Ala Ala Ala Gln Ser Gln Val Gln
                275                 280                 285

Val Leu Lys Glu Lys Lys Gln Ala Thr Glu Arg Leu Val Ser Leu
                290                 295                 300

Ser Ala Gln Ser Glu Lys Arg Leu Gln Glu Leu Glu Arg Asn Val
                305                 310                 315

Gln Leu Met Arg Gln Gln Gln Gly Gln Leu Gln Arg Arg Leu Arg
                320                 325                 330

Glu Glu Thr Glu Gln Lys Arg Arg Leu Glu Ala Glu Met Ser Lys
                335                 340                 345

Arg Gln His Arg Val Lys Glu Leu Glu Leu Lys His Glu Gln Gln
                350                 355                 360

Gln Lys Ile Leu Lys Ile Lys Thr Glu Glu Ile Ala Ala Phe Gln
                365                 370                 375

Arg Lys Arg Arg Ser Gly Ser Asn Gly Ser Val Val Ser Leu Glu
                380                 385                 390

Gln Gln Gln Lys Ile Glu Glu Gln Lys Lys Trp Leu Asp Gln Glu
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8

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Met Glu Lys Val Leu Gln Gln Arg Arg Ala Leu Glu Glu Leu Gly
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Glu Glu Leu His Lys Arg Glu Ala Ile Leu Ala Lys Lys Glu Ala
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Leu Met Gln Glu Lys Thr Gly Leu Glu Ser Lys Arg Leu Arg Ser
            440   445   450

Ser Gln Ala Leu Asn Glu Asp Ile Val Arg Val Ser Ser Arg Leu
            455   460   465

Glu His Leu Glu Lys Glu Leu Ser Glu Lys Ser Gly Gln Leu Arg
            470   475   480

Gln Gly Ser Ala Gln Ser Gln Gln Gln Ile Arg Gly Glu Ile Asp
            485   490   495

Ser Leu Arg Gln Glu Lys Asp Ser Leu Leu Lys Gln Arg Leu Glu
            500   505   510

Ile Asp Gly Lys Leu Arg Gln Gly Ser Leu Leu Ser Pro Glu Glu
            515   520   525

Glu Arg Thr Leu Phe Gln Leu Asp Glu Ala Ile Glu Ala Leu Asp
            530   535   540

Ala Ala Ile Glu Tyr Lys Asn Glu Ala Ile Thr Cys Arg Gln Arg
            545   550   555

Val Leu Arg Ala Ser Ala Ser Leu Leu Ser Gln Cys Glu Met Asn
            560   565   570

Leu Met Ala Lys Leu Ser Tyr Leu Ser Ser Ser Glu Thr Arg Ala
            575   · 580   585

Leu Leu Cys Lys Tyr Phe Asp Lys Val Val Thr Leu Arg Glu Glu
            590   595   600

Gln His Gln Gln Gln Ile Ala Phe Ser Glu Leu Glu Met Gln Leu
            605   610   615

Glu Glu Gln Gln Arg Leu Val Tyr Trp Leu Glu Val Ala Leu Glu
            620   625   630

Arg Gln Arg Leu Glu Met Asp Arg Gln Leu Thr Leu Gln Gln Lys
            635   640   645

Glu His Glu Gln Asn Met Gln Leu Leu Gln Gln Ser Arg Asp
            650   655   660

His Leu Gly Glu Gly Leu Ala Asp Ser Arg Arg Gln Tyr Glu Ala
            665   670   675

Arg Ile Gln Ala Leu Glu Lys Glu Leu Gly Arg Tyr Met Trp Ile
            680   685   690

Asn Gln Glu Leu Lys Gln Lys Leu Gly Gly Val Asn Ala Val Gly
                695   700   705

His Ser Arg Gly Gly Glu Lys Arg Ser Leu Cys Ser Glu Gly Arg
                710   715   720

Gln Ala Pro Gly Asn Glu Asp Glu Leu His Leu Ala Pro Glu Leu
                725   730   735

Leu Trp Leu Ser Pro Leu Thr Glu Gly Ala Pro Arg Thr Arg Glu
                740   745   750

Glu Thr Arg Asp Leu Val His Ala Pro Leu Pro Leu Thr Trp Lys
                755   760   765

Arg Ser Ser Leu Cys Gly Glu Glu Gln Gly Ser Pro Glu Glu Leu
                770   775   780

Arg Gln Arg Glu Ala Ala Glu Pro Leu Val Gly Arg Val Leu Pro
                785   790   795

Val Gly Glu Ala Gly Leu Pro Trp Asn Phe Gly Pro Leu Ser Lys
                800   805   810

Pro Arg Arg Glu Leu Arg Arg Ala Ser Pro Gly Met Ile Asp Val
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Arg Lys Asn Pro Leu
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<211> 662
<212> DNA
<213> Homo sapiens

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gtgtgggaac aagatctaca acccttcaga gcagtgctgt tatgatgatg 200

ccatcttatc cttaaaggag acccgccgct gtggctccac ctgcaccttc 250

tggccctgct ttgagctctg ctgtcccgag tcttttggcc cccagcagaa 300

gtttcttgtg aagttgaggg ttctgggtat gaagtctcag tgtcacttat 350

ctcccatctc ccggagctgt accaggaaca ggaggcacgt cctgtaccca 400

taaaaacccc aggctccact ggcagacggc agacaagggg agaagagacg 450

aagcagctgg acatcggaga ctacagttga acttcggaga gaagcaactt 500

gacttcagag ggatggctca atgacatagc tttggagagg agcccagctg 550

10

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gggatggcca gacttcaggg gaagaatgcc ttcctgcttc atccccttc 600

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catttaccat ct 662
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<210> 9
<211> 125
<212> PRT
<213> Homo sapiens

<400> 9
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Val Phe Leu Leu Gln Cys Ser Lys Gly Thr Thr Asp Ala Pro Val
                 20                  25                  30

Gly Ser Gly Leu Trp Leu Cys Gln Pro Thr Pro Arg Cys Gly Asn
                 35                  40                  45

Lys Ile Tyr Asn Pro Ser Glu Gln Cys Cys Tyr Asp Asp Ala Ile
                 50                  55                  60

Leu Ser Leu Lys Glu Thr Arg Arg Cys Gly Ser Thr Cys Thr Phe
                 65                  70                  75

Trp Pro Cys Phe Glu Leu Cys Cys Pro Glu Ser Phe Gly Pro Gln
                 80                  85                  90

Gln Lys Phe Leu Val Lys Leu Arg Val Leu Gly Met Lys Ser Gln
                 95                  100                 105

Cys His Leu Ser Pro Ile Ser Arg Ser Cys Thr Arg Asn Arg Arg
                 110                 115                 120

His Val Leu Tyr Pro
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<210> 10
<211> 1942
<212> DNA
<213> Homo sapiens

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ctgccgggtc tggagagctc cccgaacccc tccgcggaga ggagcgaggc 150

ggcgccaggg tggcccccgg ggcgcgcttg gtctcggaga agcggggacg 200

aggccggagg atgagcgact gagggcgacg cgggcactga cgcgagttgg 250

ggccgcgact accggcagct gacagcgcga tgagcgactc cccagagacg 300

ccctagcccg gtgtgcgcgc caggcggagc gcgcaggtgg ggctgggctg 350
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11

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ggcagttggc gcgctctcca gttccctcct ggtcacctgc tgcctgatgg 650

tggctctgtg cagtccgagc atcccgctgg agaagctggc ccaggcacca 700

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gcgggtgaac gagctcgggc gcccggcgag ggacgagggc ggcagcggcc 800

gggactggaa gagcaagagc ggccgtgggc tcgccggccg tgagccgtgg 850

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ggatctgcag gtccggcccc gcggggacac cccgcaggcg gaagccctgg 950

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ccacccgagg agtacgtgta cccggactac cgtggcaagg gctgcgtgga 1050

cgagagcggc ttcgtgtacg cgatcgggga gaagttcgcg ccgggcccct 1100

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tactgatgtg aacattctag atgactctgg gaactatcag tcaaagaaga 1650

cttttgatga ggaataatgg aaaattgttg gtacttttcc ttttcttgat 1700

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aactttgggc ataaaatcct tctctaaata aatgtgctat tttcacagta 1800
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12

agtacacaaa agtacactat tatatatcaa atgtatttct ataatccctc 1850

cattagagag cttatataag tgttttctat agatgcagat taaaaatgct 1900

gtgttgtcaa ccgtcaaaaa aaaaaaaaaa aaaaaaaaaa aa 1942

<210> 11
<211> 325
<212> PRT
<213> Homo sapiens

<400> 11
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Leu Leu Val Thr Cys Cys Leu Met Val Ala Leu Cys Ser Pro Ser
                20              25                  30

Ile Pro Leu Glu Lys Leu Ala Gln Ala Pro Glu Gln Pro Gly Gln
                35              40                  45

Glu Lys Arg Glu His Ala Thr Arg Asp Gly Pro Gly Arg Val Asn
                50              55                  60

Glu Leu Gly Arg Pro Ala Arg Asp Glu Gly Gly Ser Gly Arg Asp
                65              70                  75

Trp Lys Ser Lys Ser Gly Arg Gly Leu Ala Gly Arg Glu Pro Trp
                80              85                  90

Ser Lys Leu Lys Gln Ala Trp Val Ser Gln Gly Gly Gly Ala Lys
                95              100                 105

Ala Gly Asp Leu Gln Val Arg Pro Arg Gly Asp Thr Pro Gln Ala
                110             115                 120

Glu Ala Leu Ala Ala Ala Ala Gln Asp Ala Ile Gly Pro Glu Leu
                125             130                 135

Ala Pro Thr Pro Glu Pro Pro Glu Glu Tyr Val Tyr Pro Asp Tyr
                140             145                 150

Arg Gly Lys Gly Cys Val Asp Glu Ser Gly Phe Val Tyr Ala Ile
                155             160                 165

Gly Glu Lys Phe Ala Pro Gly Pro Ser Ala Cys Pro Cys Leu Cys
                170             175                 180

Thr Glu Glu Gly Pro Leu Cys Ala Gln Pro Glu Cys Pro Arg Leu
                185             190                 195

His Pro Arg Cys Ile His Val Asp Thr Ser Gln Cys Cys Pro Gln
                200             205                 210

Cys Lys Glu Arg Lys Asn Tyr Cys Glu Phe Arg Gly Lys Thr Tyr
                215             220                 225

Gln Thr Leu Glu Glu Phe Val Val Ser Pro Cys Glu Arg Cys Arg
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13

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                    230                 235                 240
        Cys Glu Ala Asn Gly Glu Val Leu Cys Thr Val Ser Ala Cys Pro
                    245                 250                 255

        Gln Thr Glu Cys Val Asp Pro Val Tyr Glu Pro Asp Gln Cys Cys
                    260                 265                 270

        Pro Ile Cys Lys Asn Gly Pro Asn Cys Phe Ala Glu Thr Ala Val
                    275                 280                 285

        Ile Pro Ala Gly Arg Glu Val Lys Thr Asp Glu Cys Thr Ile Cys
                    290                 295                 300

        His Cys Thr Tyr Glu Glu Gly Thr Trp Arg Ile Glu Arg Gln Ala
                    305                 310                 315

        Met Cys Thr Arg His Glu Cys Arg Gln Met
                    320                 325
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<210> 12
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 12
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<210> 13
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 13
 cgctcgattc tccatgtgcc ttcc 24

<210> 14
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 14
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<210> 15
<211> 1587
<212> DNA
<213> Homo sapiens

14

<400> 15

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gttcagcatg tgtggaaggt gtccgaccta ccccggcaat ggacccctaa 150

gaacaccagc tgcgacagcg gcttggggtg ccaggacacg ttgatgctca 200

ttgagagcgg accccaagtg agcctggtgc tctccaaggg ctgcacggag 250

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tcctcaggct caggggagga ggcatcttct ccaatctgag agtccaggga 550

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gcccgtgggt atgactgaga actgcaatag gaaagatttt ctgacctgtc 650

atcggggac caccattatg acacacggaa acttggctca agaacccact 700

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aatggccttg gacaccagat tctttcccat tctgtccatg aatcatcttc 1450

15

cccacacaca atcattcata tctactcacc taacagcaac actggggaga 1500

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gctgcatgta tctgataata cagaccctgt cctttca 1587

<210> 16
<211> 437
<212> PRT
<213> Homo sapiens

<400> 16

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Met Ser Ala Val Leu Leu Leu Ala Leu Leu Gly Phe Ile Leu Pro
 1               5                   10                  15

Leu Pro Gly Val Gln Ala Leu Leu Cys Gln Phe Gly Thr Val Gln
                20              25                  30

His Val Trp Lys Val Ser Asp Leu Pro Arg Gln Trp Thr Pro Lys
                35                  40                  45

Asn Thr Ser Cys Asp Ser Gly Leu Gly Cys Gln Asp Thr Leu Met
                50                  55                  60

Leu Ile Glu Ser Gly Pro Gln Val Ser Leu Val Leu Ser Lys Gly
                65                  70                  75

Cys Thr Glu Ala Lys Asp Gln Glu Pro Arg Val Thr Glu His Arg
                80                  85                  90

Met Gly Pro Gly Leu Ser Leu Ile Ser Tyr Thr Phe Val Cys Arg
                95                  100                 105

Gln Glu Asp Phe Cys Asn Asn Leu Val Asn Ser Leu Pro Leu Trp
                110                 115                 120

Ala Pro Gln Pro Pro Ala Asp Pro Gly Ser Leu Arg Cys Pro Val
                125                 130                 135

Cys Leu Ser Met Glu Gly Cys Leu Glu Gly Thr Thr Glu Glu Ile
                140                 145                 150

Cys Pro Lys Gly Thr Thr His Cys Tyr Asp Gly Leu Leu Arg Leu
                155                 160                 165

Arg Gly Gly Gly Ile Phe Ser Asn Leu Arg Val Gln Gly Cys Met
                170                 175                 180

Pro Gln Pro Gly Cys Asn Leu Leu Asn Gly Thr Gln Glu Ile Gly
                185                 190                 195

Pro Val Gly Met Thr Glu Asn Cys Asn Arg Lys Asp Phe Leu Thr
                200                 205                 210

Cys His Arg Gly Thr Thr Ile Met Thr His Gly Asn Leu Ala Gln
                215                 220                 225

Glu Pro Thr Asp Trp Thr Thr Ser Asn Thr Glu Met Cys Glu Val
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16

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      Gly Gln Val Cys Gln Glu Thr Leu Leu Leu Ile Asp Val Gly Leu
                      245                    250                    255

      Thr Ser Thr Leu Val Gly Thr Lys Gly Cys Ser Thr Val Gly Ala
                      260                    265                    270

      Gln Asn Ser Gln Lys Thr Thr Ile His Ser Ala Pro Pro Gly Val
                      275                    280                    285

      Leu Val Ala Ser Tyr Thr His Phe Cys Ser Ser Asp Leu Cys Asn
                      290                    295                    300

      Ser Ala Ser Ser Ser Ser Val Leu Leu Asn Ser Leu Pro Pro Gln
                      305                    310                    315

      Ala Ala Pro Val Pro Gly Asp Arg Gln Cys Pro Thr Cys Val Gln
                      320                    325                    330

      Pro Leu Gly Thr Cys Ser Ser Gly Ser Pro Arg Met Thr Cys Pro
                      335                    340                    345

      Arg Gly Ala Thr His Cys Tyr Asp Gly Tyr Ile His Leu Ser Gly
                      350                    355                    360

      Gly Gly Leu Ser Thr Lys Met Ser Ile Gln Gly Cys Val Ala Gln
                      365                    370                    375

      Pro Ser Ser Phe Leu Leu Asn His Thr Arg Gln Ile Gly Ile Phe
                      380                    385                    390

      Ser Ala Arg Glu Lys Arg Asp Val Gln Pro Pro Ala Ser Gln His
                      395                    400                    405

      Glu Gly Gly Gly Ala Glu Gly Leu Glu Ser Leu Thr Trp Gly Val
                      410                    415                    420

      Gly Leu Ala Leu Ala Pro Ala Leu Trp Trp Gly Val Val Cys Pro
                      425                    430                    435

      Ser Cys
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<210> 17
<211> 2387
<212> DNA
<213> Homo sapiens

<400> 17
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  gccgcggccc tggctgcggc gctgctctcg tcgcttgcgc gctgctctct 100

  tctagagccg agggacccgg tggcctcgtc gctcagcccc tatttcggca 150

  ccaagactcg ctacgaggat gtcaaccccg tgctattgtc gggccccgag 200
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gctccgtggc gggaccctga gctgctggag gggacctgca ccccggtgca 250

gctggtcgcc ctcattcgcc acggcacccg ctaccccacg gtcaaacaga 300

tccgcaagct gaggcagctg cacgggttgc tgcaggcccg cgggtccagg 350

gatggcgggg ctagtagtac cggcagccgc gacctgggtg cagcgctggc 400

cgactggcct ttgtggtacg cggactggat ggacgggcag ctagtagaga 450

agggacggca ggatatgcga cagctggcgc tgcgtctggc ctcgctcttc 500

ccggcccttt tcagccgtga gaactacggc cgcctgcggc tcatcaccag 550

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ggcagcacta ccaccctggc ttgccgccgc cggacgtcgc agatatggag 650

tttggacctc caacagttaa tgataaacta atgagatttt ttgatcactg 700

tgagaagttt ttaactgaag tagaaaaaaa tgctacagct ctttatcacg 750

tggaagcctt caaaactgga ccagaaatgc agaacatttt aaaaaaagtt 800

gcagctactt tgcaagtgcc agtaaatgat ttaaatgcag atttaattca 850

agtagccttt ttcacctgtt catttgacct ggcaattaaa ggtgttaaat 900

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ttaaatgatc tgaaacaata ttggaaaaga ggatatgggt atactattaa 1000

cagtcgatcc agctgcacct tgtttcagga tatctttcag cacttggaca 1050

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ctacttcaaa gacaaggaac ccctaacagc gtacaattac aaaaaacaaa 1200

tgcatcggaa gttccgaagt ggtctcattg taccttatgc ctcgaacctg 1250

atatttgtgc tttaccactg tgaaaatgct aagactccta agaacaatt 1300

ccgagtgcag atgttattaa atgaaaaggt gttacctttg gcttactcac 1350

aagaaactgt ttcattttat gaagatctga agaaccacta caaggacatc 1400

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tcacactgag atagaattgt gatttcataa taacacttga aaagtgctgg 1800

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cagctctagc attttcttaa tcaggaatat tgtggtaagc tgggagtatc 1950

actctggaag aaagtaacat ctccagatga gaatttgaaa caagaaacag 2000

agtgttgtaa aaggacacct tcactgaagc aagtcggaaa gtacaatgaa 2050

aataaatatt tttggtattt atttatgaaa tatttgaaca tttttttcaat 2100

aattcctttt tacttctagg aagtctcaaa agaccatctt aaattattat 2150

atgtttggac aattagcaac aagtcagata gttagaatcg aagtttttca 2200

aatccattgc ttagctaact ttttcattct gtcacttggc ttcgattttt 2250

atattttcct attatatgaa atgtatcttt tggttgtttg attttttcttt 2300

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ctataataaa gaaaattctt gtgactttaa aaaaaaa 2387
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<210> 18
<211> 487
<212> PRT
<213> Homo sapiens

<400> 18
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Met Leu Arg Ala Pro Gly Cys Leu Leu Arg Thr Ser Val Ala Pro
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Ala Ala Ala Leu Ala Ala Ala Leu Leu Ser Ser Leu Ala Arg Cys
                20                  25                  30

Ser Leu Leu Glu Pro Arg Asp Pro Val Ala Ser Ser Leu Ser Pro
                35                  40                  45

Tyr Phe Gly Thr Lys Thr Arg Tyr Glu Asp Val Asn Pro Val Leu
                50                  55                  60

Leu Ser Gly Pro Glu Ala Pro Trp Arg Asp Pro Glu Leu Leu Glu
                65                  70                  75

Gly Thr Cys Thr Pro Val Gln Leu Val Ala Leu Ile Arg His Gly
                80                  85                  90

Thr Arg Tyr Pro Thr Val Lys Gln Ile Arg Lys Leu Arg Gln Leu
                95                  100                 105

His Gly Leu Leu Gln Ala Arg Gly Ser Arg Asp Gly Gly Ala Ser
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                    110                    115                    120
Ser Thr Gly Ser Arg Asp Leu Gly Ala Ala Leu Ala Asp Trp Pro
                    125                    130                    135

Leu Trp Tyr Ala Asp Trp Met Asp Gly Gln Leu Val Glu Lys Gly
                    140                    145                    150

Arg Gln Asp Met Arg Gln Leu Ala Leu Arg Leu Ala Ser Leu Phe
                    155                    160                    165

Pro Ala Leu Phe Ser Arg Glu Asn Tyr Gly Arg Leu Arg Leu Ile
                    170                    175                    180

Thr Ser Ser Lys His Arg Cys Met Asp Ser Ser Ala Ala Phe Leu
                    185                    190                    195

Gln Gly Leu Trp Gln His Tyr His Pro Gly Leu Pro Pro Pro Asp
                    200                    205                    210

Val Ala Asp Met Glu Phe Gly Pro Pro Thr Val Asn Asp Lys Leu
                    215                    220                    225

Met Arg Phe Phe Asp His Cys Glu Lys Phe Leu Thr Glu Val Glu
                    230                    235                    240

Lys Asn Ala Thr Ala Leu Tyr His Val Glu Ala Phe Lys Thr Gly
                    245                    250                    255

Pro Glu Met Gln Asn Ile Leu Lys Lys Val Ala Ala Thr Leu Gln
                    260                    265                    270

Val Pro Val Asn Asp Leu Asn Ala Asp Leu Ile Gln Val Ala Phe
                    275                    280                    285

Phe Thr Cys Ser Phe Asp Leu Ala Ile Lys Gly Val Lys Ser Pro
                    290                    295                    300

Trp Cys Asp Val Phe Asp Ile Asp Asp Ala Lys Val Leu Glu Tyr
                    305                    310                    315

Leu Asn Asp Leu Lys Gln Tyr Trp Lys Arg Gly Tyr Gly Tyr Thr
                    320                    325                    330

Ile Asn Ser Arg Ser Ser Cys Thr Leu Phe Gln Asp Ile Phe Gln
                    335                    340                    345

His Leu Asp Lys Ala Val Glu Gln Lys Gln Arg Ser Gln Pro Ile
                    350                    355                    360

Ser Ser Pro Val Ile Leu Gln Phe Gly His Ala Glu Thr Leu Leu
                    365                    370                    375

Pro Leu Leu Ser Leu Met Gly Tyr Phe Lys Asp Lys Glu Pro Leu
                    380                    385                    390

Thr Ala Tyr Asn Tyr Lys Lys Gln Met His Arg Lys Phe Arg Ser
                    395                    400                    405
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20

Gly Leu Ile Val Pro Tyr Ala Ser Asn Leu Ile Phe Val Leu Tyr
            410   415   420

His Cys Glu Asn Ala Lys Thr Pro Lys Glu Gln Phe Arg Val Gln
            425   430   435

Met Leu Leu Asn Glu Lys Val Leu Pro Leu Ala Tyr Ser Gln Glu
            440   445   450

Thr Val Ser Phe Tyr Glu Asp Leu Lys Asn His Tyr Lys Asp Ile
            455   460   465

Leu Gln Ser Cys Gln Thr Ser Glu Glu Cys Glu Leu Ala Arg Ala
            470   475   480

Asn Ser Thr Ser Asp Glu Leu
            485

<210> 19
<211> 3554
<212> DNA
<213> Homo sapiens

<400> 19
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cttcttcctg ctgctgcttt tcaggggctg cctgataggg gctgtaaatc 150

tcaaatccag caatcgaacc ccagtggtac aggaatttga aagtgtggaa 200

ctgtcttgca tcattacgga ttcgcagaca agtgacccca ggatcgagtg 250

gaagaaaatt caagatgaac aaaccacata tgtgtttttt gacaacaaaa 300

ttcagggaga cttggcgggt cgtgcagaaa tactggggaa gacatccctg 350

aagatctgga atgtgacacg gagagactca gccctttatc gctgtgaggt 400

cgttgctcga aatgaccgca aggaaattga tgagattgtg atcgagttaa 450

ctgtgcaagt gaagccagtg accctgtct gtagagtgcc gaaggctgta 500

ccagtaggca agatggcaac actgcactgc caggagagtg agggccaccc 550

ccggcctcac tacagctggt atcgcaatga tgtaccactg cccacggatt 600

ccagagccaa tcccagattt cgcaattctt ctttccactt aaactctgaa 650

acaggcactt tggtgttcac tgctgttcac aaggacgact ctgggcagta 700

ctactgcatt gcttccaatg acgcaggctc agccaggtgt gaggagcagg 750

agatggaagt ctatgacctg aacattggcg gaattattgg ggggggttctg 800

gttgtccttg ctgtactggc cctgatcacg ttgggcatct gctgtgcata 850

21

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gacttcagac acaagtcatc gtttgtgatc tgagacccgc ggtgtggctg 1000

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ttttacccaa ggaatcctct catggaagtt tactgtgatg ttccttttct 1950

cacacaagtt ttagcctttt tcacaaggga actcatactg tctacacatc 2000

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gcctcttcct gagatgacta ggacagtctg tacccagagg ccacccagaa 2150

gccctcagat gtacatacac agatgccagt cagctcctgg ggttgcgcca 2200

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22

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cccactgttc ctctttgcca cagagaaagc acccagacgc cacaggctct 2600

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tgaaacgcct gaatcaaaag cagttttcta attttgactt taaattttc 2750

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aagatatgaa tgtgactcaa gactcgaggc cgatacgagg ctgtgattct 3450

gcctttggat ggatgttgct gtacacagat gctacagact tgtactaaca 3500

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ccca 3554
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<210> 20
<211> 310
<212> PRT
<213> Homo sapiens

<400> 20

23

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               20   25   30

Ala Val Asn Leu Lys Ser Ser Asn Arg Thr Pro Val Val Gln Glu
               35   40   45

Phe Glu Ser Val Glu Leu Ser Cys Ile Ile Thr Asp Ser Gln Thr
               50   55   60

Ser Asp Pro Arg Ile Glu Trp Lys Lys Ile Gln Asp Glu Gln Thr
               65   70   75

Thr Tyr Val Phe Phe Asp Asn Lys Ile Gln Gly Asp Leu Ala Gly
               80   85   90

Arg Ala Glu Ile Leu Gly Lys Thr Ser Leu Lys Ile Trp Asn Val
               95   100   105

Thr Arg Arg Asp Ser Ala Leu Tyr Arg Cys Glu Val Val Ala Arg
              110   115   120

Asn Asp Arg Lys Glu Ile Asp Glu Ile Val Ile Glu Leu Thr Val
              125   130   135

Gln Val Lys Pro Val Thr Pro Val Cys Arg Val Pro Lys Ala Val
              140   145   150

Pro Val Gly Lys Met Ala Thr Leu His Cys Gln Glu Ser Glu Gly
              155   160   165

His Pro Arg Pro His Tyr Ser Trp Tyr Arg Asn Asp Val Pro Leu
              170   175   180

Pro Thr Asp Ser Arg Ala Asn Pro Arg Phe Arg Asn Ser Ser Phe
              185   190   195

His Leu Asn Ser Glu Thr Gly Thr Leu Val Phe Thr Ala Val His
              200   205   210

Lys Asp Asp Ser Gly Gln Tyr Tyr Cys Ile Ala Ser Asn Asp Ala
              215   220   225

Gly Ser Ala Arg Cys Glu Glu Gln Glu Met Glu Val Tyr Asp Leu
              230   235   240

Asn Ile Gly Gly Ile Ile Gly Gly Val Leu Val Val Leu Ala Val
              245   250   255

Leu Ala Leu Ile Thr Leu Gly Ile Cys Cys Ala Tyr Arg Arg Gly
              260   265   270

Tyr Phe Ile Asn Asn Lys Gln Asp Gly Glu Ser Tyr Lys Asn Pro
              275   280   285

Gly Lys Pro Asp Gly Val Asn Tyr Ile Arg Thr Asp Glu Glu Gly

24

290   295   300

        Asp Phe Arg His Lys Ser Ser Phe Val Ile
                        305   310

<210> 21
<211> 3437
<212> DNA
<213> Homo sapiens

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    gagaagccac tgcccaccgc cttcctggtg gacacatcgg aggaggcgct   200

    gctgcttcct gactggctga gctgcgcat gatccgttct gaggtgctcc   250

    gcctggtgga cgccgccctg caggacctgg agccgcagca gctgctgctg   300

    ttcgtgcagt cgtttggcat ccccgtgtcc agcatgagca aactcctcca   350

    gttcctggac caggcagtgg cccacgaccc ccagactctg gagcagaaca   400

    tcatggacaa gaattacatg gcccacctgg tggaggtcca gcatgagcgc   450

    ggcgcctccg gaggccagac tttccactcc ttgctcacag cctccctgcc   500

    gccccgccga cagcacag aggcacccaa accaaagagc agcccagagc   550

    agcccatagg ccagggccgg attcgggtgg ggacccagct ccgggtgctg   600

    ggccctgagg acgacctggc tggcatgttc ctccagattt tcccgctcag   650

    cccggaccct cggtggcaga gctccagtcc ccgccccgtg gccctcgccc   700

    tgcagcaggc cctgggccag gagctggccc gcgtcgtcca gggcagcccc   750

    gaggtgccgg gcatcacggt gcgtgtcctg caggccctcg ccaccctgct   800

    cagctcccca cacggcggtg ccctggtgat gtccatgcac cgtagccact   850

    tcctggcctg cccgctgctg cgccagctct gccagtacca gcgctgtgtg   900

    ccacaggaca ccggcttctc ctcgctcttc ctgaaggtgc tcctgcagat   950

    gctgcagtgg ctggacagcc ctggcgtgga gggcgggccc ctgcgggcac 1000

    agctcaggat gcttgccagc caggcctcag ccgggcgcag gctcagtgat 1050

    gtgcgagggg ggctcctgcg cctggccgag gccctggcct tccgtcagga 1100

    cctggaggtg gtcagctcca ccgtccgtgc cgtcatcgcc accctgaggt 1150

    ctggggagca gtgcagcgtg gagccggacc tgatcagcaa agtcctccag 1200

                                25

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gggctgatcg aggtgaggtc cccccacctg gaggagctgc tgactgcatt 1250

cttctctgcc actgcggatg ctgcctcccc gtttccagcc tgtaagcccg 1300

ttgtggtggt gagctccctg ctgctgcagg aggaggagcc cctggctggg 1350

gggaagccgg gtgcggacgg tggcagcctg gaggccgtgc ggctggggcc 1400

ctcgtcaggc ctcctagtgg actggctgga aatgctggac cccgaggtgg 1450

tcagcagctg ccccgacctg cagctcaggc tgctcttctc ccggaggaag 1500

ggcaaaggtc aggcccaggt gccctcgttc cgtccctacc tcctgaccct 1550

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ttcctctggg cctgcatcca tgttcctcgc atctggcagg ggcgggacca 1700

gcgcaccccg cagaagcggc gggaggagct ggtgctgcgg gtccagggcc 1750

cggagctcat cagcctggtg gagctgatcc tggccgaggc ggagacgcgg 1800

agccaggacg gggacacagc cgcctgcagc ctcatccagg cccggctgcc 1850

cctgctgctc agctgctgct gtggggacga tgagagtgtc aggaaggtga 1900

cggagcacct gtcaggctgc atccagcagt ggggagacag cgtgctggga 1950

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gcagcgtctg caagctggac ggactcatcc accgcttcat cacgctcctt 2100

gcggacacca gcgactcccg ggcgttggag aaccgagggg cggatgccag 2150

catggcctgc cggaagctgg cggtggcgca cccgctgctg ctgctcaggc 2200

acctgcccat gatcgcggcg ctcctgcacg gccgcaccca cctcaacttc 2250

caggagttcc ggcagcagaa ccacctgagc tgcttcctgc acgtgctggg 2300

cctgctggag ctgctgcagc cgcacgtgtt ccgcagcgag caccaggggg 2350

cgctgtggga ctgccttctg tccttcatcc gcctgctgct gaattacagg 2400

aagtcctccc gccatctggc tgccttcatc aacaagtttg tgcagttcat 2450

ccataagtac attacctaca atgccccagc agccatctcc ttcctgcaga 2500

agcacgccga cccgctccac gacctgtcct tcgacaacag tgacctggtg 2550

atgctgaaat ccctccttgc agggctcagc ctgcccagca gggacgacag 2600

gaccgaccga ggcctggacg aagagggcga ggaggagagc tcagccggct 2650
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26

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ccttgcccct ggtcagcgtc tccctgttca cccctctgac cgcggccgag 2700

atggccccct acatgaaacg gctttcccgg ggccaaacgg tggaggatct 2750

gctggaggtt ctgagtgaca tagacgagat gtcccggcgg agacccgaga 2800

tcctgagctt cttctcgacc aacctgcagc ggctgatgag ctcggccgag 2850

gagtgttgcc gcaacctcgc cttcagcctg ccctgcgct ccatgcagaa 2900

cagccccagc attgcagccg ctttcctgcc cacgttcatg tactgcctgg 2950

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tacgctctcc tgtgccaaga gcacgcggct gtgctgctcc accgggcctt 3050

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cccccctcca agccccggcc cgtcccgtcc ccggggatcc tcgaggcaaa 3200

gcccaggaag cgtgggcgtt gctggtctgt ccgaggaggt gagggcgccg 3250

agccctgagg ccaggcaggc ccaggagcaa tactccgagc cctggggtgg 3300

ctccgggccg gccgctggca tcaggggccg tccagcaagc cctcattcac 3350

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<210> 22
<211> 1029
<212> PRT
<213> Homo sapiens

<400> 22
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Met His Ile Leu Val Val His Ala Met Val Ile Leu Leu Thr Leu
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Gly Pro Pro Arg Ala Asp Asp Ser Glu Phe Gln Ala Leu Leu Asp
              20                  25                  30

Ile Trp Phe Pro Glu Glu Lys Pro Leu Pro Thr Ala Phe Leu Val
              35                  40                  45

Asp Thr Ser Glu Glu Ala Leu Leu Leu Pro Asp Trp Leu Lys Leu
              50                  55                  60

Arg Met Ile Arg Ser Glu Val Leu Arg Leu Val Asp Ala Ala Leu
              65                  70                  75

Gln Asp Leu Glu Pro Gln Gln Leu Leu Leu Phe Val Gln Ser Phe
              80                  85                  90

Gly Ile Pro Val Ser Ser Met Ser Lys Leu Leu Gln Phe Leu Asp
                  95                  100                 105
```

27

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Gln Ala Val Ala His Asp Pro Gln Thr Leu Glu Gln Asn Ile Met
            110                 115                 120

Asp Lys Asn Tyr Met Ala His Leu Val Glu Val Gln His Glu Arg
            125                 130                 135

Gly Ala Ser Gly Gly Gln Thr Phe His Ser Leu Leu Thr Ala Ser
            140                 145                 150

Leu Pro Pro Arg Arg Asp Ser Thr Glu Ala Pro Lys Pro Lys Ser
            155                 160                 165

Ser Pro Glu Gln Pro Ile Gly Gln Gly Arg Ile Arg Val Gly Thr
            170                 175                 180

Gln Leu Arg Val Leu Gly Pro Glu Asp Asp Leu Ala Gly Met Phe
            185                 190                 195

Leu Gln Ile Phe Pro Leu Ser Pro Asp Pro Arg Trp Gln Ser Ser
            200                 205                 210

Ser Pro Arg Pro Val Ala Leu Ala Leu Gln Gln Ala Leu Gly Gln
            215                 220                 225

Glu Leu Ala Arg Val Val Gln Gly Ser Pro Glu Val Pro Gly Ile
            230                 235                 240

Thr Val Arg Val Leu Gln Ala Leu Ala Thr Leu Leu Ser Ser Pro
            245                 250                 255

His Gly Gly Ala Leu Val Met Ser Met His Arg Ser His Phe Leu
            260                 265                 270

Ala Cys Pro Leu Leu Arg Gln Leu Cys Gln Tyr Gln Arg Cys Val
            275                 280                 285

Pro Gln Asp Thr Gly Phe Ser Ser Leu Phe Leu Lys Val Leu Leu
            290                 295                 300

Gln Met Leu Gln Trp Leu Asp Ser Pro Gly Val Glu Gly Gly Pro
            305                 310                 315

Leu Arg Ala Gln Leu Arg Met Leu Ala Ser Gln Ala Ser Ala Gly
            320                 325                 330

Arg Arg Leu Ser Asp Val Arg Gly Gly Leu Leu Arg Leu Ala Glu
            335                 340                 345

Ala Leu Ala Phe Arg Gln Asp Leu Glu Val Val Ser Ser Thr Val
            350                 355                 360

Arg Ala Val Ile Ala Thr Leu Arg Ser Gly Glu Gln Cys Ser Val
            365                 370                 375

Glu Pro Asp Leu Ile Ser Lys Val Leu Gln Gly Leu Ile Glu Val
            380                 385                 390

Arg Ser Pro His Leu Glu Glu Leu Leu Thr Ala Phe Phe Ser Ala
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Thr Ala Asp Ala Ala Ser Pro Phe Pro Ala Cys Lys Pro Val Val
                410   415   420

Val Val Ser Ser Leu Leu Leu Gln Glu Glu Glu Pro Leu Ala Gly
                425   430   435

Gly Lys Pro Gly Ala Asp Gly Gly Ser Leu Glu Ala Val Arg Leu
                440   445   450

Gly Pro Ser Ser Gly Leu Leu Val Asp Trp Leu Glu Met Leu Asp
                455   460   465

Pro Glu Val Val Ser Ser Cys Pro Asp Leu Gln Leu Arg Leu Leu
                470   475   480

Phe Ser Arg Arg Lys Gly Lys Gly Gln Ala Gln Val Pro Ser Phe
                485   490   495

Arg Pro Tyr Leu Leu Thr Leu Phe Thr His Gln Ser Ser Trp Pro
                500   505   510

Thr Leu His Gln Cys Ile Arg Val Leu Leu Gly Lys Ser Arg Glu
                515   520   525

Gln Arg Phe Asp Pro Ser Ala Ser Leu Asp Phe Leu Trp Ala Cys
                530   535   540

Ile His Val Pro Arg Ile Trp Gln Gly Arg Asp Gln Arg Thr Pro
                545   550   555

Gln Lys Arg Arg Glu Glu Leu Val Leu Arg Val Gln Gly Pro Glu
                560   565   570

Leu Ile Ser Leu Val Glu Leu Ile Leu Ala Glu Ala Glu Thr Arg
                575   580   585

Ser Gln Asp Gly Asp Thr Ala Ala Cys Ser Leu Ile Gln Ala Arg
                590   595   600

Leu Pro Leu Leu Leu Ser Cys Cys Cys Gly Asp Asp Glu Ser Val
                605   610   615

Arg Lys Val Thr Glu His Leu Ser Gly Cys Ile Gln Gln Trp Gly
                620   625   630

Asp Ser Val Leu Gly Arg Arg Cys Arg Asp Leu Leu Leu Gln Leu
                635   640   645

Tyr Leu Gln Arg Pro Glu Leu Arg Val Pro Val Pro Glu Val Leu
                650   655   660

Leu His Ser Glu Gly Ala Ala Ser Ser Ser Val Cys Lys Leu Asp
                665   670   675

Gly Leu Ile His Arg Phe Ile Thr Leu Leu Ala Asp Thr Ser Asp
                680   685   690

Ser Arg Ala Leu Glu Asn Arg Gly Ala Asp Ala Ser Met Ala Cys
                695   700   705

Arg Lys Leu Ala Val Ala His Pro Leu Leu Leu Leu Arg His Leu
                710   715   720

Pro Met Ile Ala Ala Leu Leu His Gly Arg Thr His Leu Asn Phe
                725   730   735

Gln Glu Phe Arg Gln Gln Asn His Leu Ser Cys Phe Leu His Val
                740   745   750

Leu Gly Leu Leu Glu Leu Leu Gln Pro His Val Phe Arg Ser Glu
                755   760   765

His Gln Gly Ala Leu Trp Asp Cys Leu Leu Ser Phe Ile Arg Leu
                770   775   780

Leu Leu Asn Tyr Arg Lys Ser Ser Arg His Leu Ala Ala Phe Ile
                785   790   795

Asn Lys Phe Val Gln Phe Ile His Lys Tyr Ile Thr Tyr Asn Ala
                800   805   810

Pro Ala Ala Ile Ser Phe Leu Gln Lys His Ala Asp Pro Leu His
                815   820   825

Asp Leu Ser Phe Asp Asn Ser Asp Leu Val Met Leu Lys Ser Leu
                830   835   840

Leu Ala Gly Leu Ser Leu Pro Ser Arg Asp Asp Arg Thr Asp Arg
                845   850   855

Gly Leu Asp Glu Glu Gly Glu Glu Glu Ser Ser Ala Gly Ser Leu
                860   865   870

Pro Leu Val Ser Val Ser Leu Phe Thr Pro Leu Thr Ala Ala Glu
                875   880   885

Met Ala Pro Tyr Met Lys Arg Leu Ser Arg Gly Gln Thr Val Glu
                890   895   900

Asp Leu Leu Glu Val Leu Ser Asp Ile Asp Glu Met Ser Arg Arg
                905   910   915

Arg Pro Glu Ile Leu Ser Phe Phe Ser Thr Asn Leu Gln Arg Leu
                920   925   930

Met Ser Ser Ala Glu Glu Cys Cys Arg Asn Leu Ala Phe Ser Leu
                935   940   945

Ala Leu Arg Ser Met Gln Asn Ser Pro Ser Ile Ala Ala Ala Phe
                950   955   960

Leu Pro Thr Phe Met Tyr Cys Leu Gly Ser Gln Asp Phe Glu Val
                965   970   975

Val Gln Thr Ala Leu Arg Asn Leu Pro Glu Tyr Ala Leu Leu Cys

30

Gln Glu His Ala Ala Val Leu Leu His Arg Ala Phe Leu Val Gly
          995   1000   1005

Met Tyr Gly Gln Met Asp Pro Ser Ala Gln Ile Ser Glu Ala Leu
          1010   1015   1020

Arg Ile Leu His Met Glu Ala Val Met
          1025

<210> 23
<211> 2186
<212> DNA
<213> Homo sapiens

<400> 23
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cgccttcctc tcgctgtcct ggtacgcggc actcagcggc cagaaaggcg 150

acgttgtgga cgtttaccag cgggagttcc tggcgctgcg cgatcggttg 200

cacgcagctg agcaggagag cctcaagcgc tccaaggagc tcaacctggt 250

gctggacgag atcaagaggg ccgtgtcaga aaggcaggcg ctgcgagacg 300

gagacggcaa tcgcacctgg ggccgcctaa cagaggaccc ccgattgaag 350

ccgtggaacg gctcacaccg gcacgtgctg cacctgccca ccgtcttcca 400

tcacctgcca cacctgctgg ccaaggagag cagtctgcag cccgcggtgc 450

gcgtgggcca gggccgcacc ggagtgtcgg tggtgatggg catcccgagc 500

gtgcggcgcg aggtgcactc gtacctgact gacactctgc actcgctcat 550

ctccgagctg agcccgcagg agaaggagga ctcggtcatc gtggtgctga 600

tcgccgagac tgactcacag tacacttcgg cagtgacaga gaacatcaag 650

gccttgttcc ccacggagat ccattctggg ctcctggagg tcatctcacc 700

ctcccccac ttctaccctg acttctcccg cctccgagag tcctttgggg 750

accccaagga gagagtcagg tggaggacca aacagaacct cgattactgc 800

ttcctcatga tgtacgcgca gtccaaaggc atctactacg tgcagctgga 850

ggatgacatc gtggccaagc ccaactacct gagcaccatg aagaactttg 900

cactgcagca gccttcagag gactggatga tcctggagtt ctcccagctg 950

ggcttcattg gtaagatgtt caagtcgctg gacctgagcc tgattgtaga 1000

gttcattctc atgttctacc gggacaagcc catcgactgg ctcctggacc 1050

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atattctgtg ggtgaaagtc tgcaaccccg agaaggatgc gaagcactgt 1100

gaccggcaga aagccaacct gcggatccgc ttcaaaccgt ccctcttcca 1150

gcacgtgggc actcactcct cgctggctgg caagatccag aaactgaagg 1200

acaaagactt tggaaagcag gcgctgcgga aggagcatgt gaacccgcca 1250

gcagaggtga gcacgagcct gaagacatac cagcacttca ccctggagaa 1300

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acttcatccg cttccgcttc ttccaacctc taagactgga gcggttcttc 1400

ttccgcagtg ggaacatcga gcacccggag acaagctct tcaacacgtc 1450

tgtggaggtg ctgcccttcg acaaccctca gtcagacaag gaggccctgc 1500

aggagggccg caccgccacc ctccggtacc ctcggagccc cgacggctac 1550

ctccagatcg gctccttcta caagggagtg gcagagggag aggtggaccc 1600

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ctgtgtgggt gattctgagc gagatcttcc tgaaaaaggc cgactaagct 1700

gcgggcttct gagggtaccc tgtggccagc cctgaagccc acatttctgg 1750

gggtgtcgtc actgccgtcc ccggagggcc agatacggcc ccgcccaaag 1800

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ggaggcccta ggagctggtg ctgcccccgc ccgccgggcc gcggaggagg 1900

caggcggccc ccacactgtg cctgaggccc ggaaccgttc gcacccggcc 1950

tgccccagtc aggccgtttt agaagagctt ttacttgggc gcccgccgtc 2000

tctggcgcga acactggaat gcatatacta ctttatgtgc tgtgtttttt 2050

attcttggat acatttgatt ttttcacgta agtccacata tacttctata 2100

agagcgtgac ttgtaataaa gggttaatga agaaaaaaaa aaaaaaaaaa 2150

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 2186
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<210> 24
<211> 548
<212> PRT
<213> Homo sapiens

<400> 24
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 Leu Cys Ala Phe Leu Ser Leu Ser Trp Tyr Ala Ala Leu Ser Gly
                 20                  25                  30
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32

Gln Lys Gly Asp Val Val Asp Val Tyr Gln Arg Glu Phe Leu Ala
            35   40   45

Leu Arg Asp Arg Leu His Ala Ala Glu Gln Glu Ser Leu Lys Arg
            50   55   60

Ser Lys Glu Leu Asn Leu Val Leu Asp Glu Ile Lys Arg Ala Val
            65   70   75

Ser Glu Arg Gln Ala Leu Arg Asp Gly Asp Gly Asn Arg Thr Trp
            80   85   90

Gly Arg Leu Thr Glu Asp Pro Arg Leu Lys Pro Trp Asn Gly Ser
            95   100   105

His Arg His Val Leu His Leu Pro Thr Val Phe His His Leu Pro
            110   115   120

His Leu Leu Ala Lys Glu Ser Ser Leu Gln Pro Ala Val Arg Val
            125   130   135

Gly Gln Gly Arg Thr Gly Val Ser Val Val Met Gly Ile Pro Ser
            140   145   150

Val Arg Arg Glu Val His Ser Tyr Leu Thr Asp Thr Leu His Ser
            155   160   165

Leu Ile Ser Glu Leu Ser Pro Gln Glu Lys Glu Asp Ser Val Ile
            170   175   180

Val Val Leu Ile Ala Glu Thr Asp Ser Gln Tyr Thr Ser Ala Val
            185   190   195

Thr Glu Asn Ile Lys Ala Leu Phe Pro Thr Glu Ile His Ser Gly
            200   205   210

Leu Leu Glu Val Ile Ser Pro Ser Pro His Phe Tyr Pro Asp Phe
            215   220   225

Ser Arg Leu Arg Glu Ser Phe Gly Asp Pro Lys Glu Arg Val Arg
            230   235   240

Trp Arg Thr Lys Gln Asn Leu Asp Tyr Cys Phe Leu Met Met Tyr
            245   250   255

Ala Gln Ser Lys Gly Ile Tyr Tyr Val Gln Leu Glu Asp Asp Ile
            260   265   270

Val Ala Lys Pro Asn Tyr Leu Ser Thr Met Lys Asn Phe Ala Leu
            275   280   285

Gln Gln Pro Ser Glu Asp Trp Met Ile Leu Glu Phe Ser Gln Leu
            290   295   300

Gly Phe Ile Gly Lys Met Phe Lys Ser Leu Asp Leu Ser Leu Ile
            305   310   315

Val Glu Phe Ile Leu Met Phe Tyr Arg Asp Lys Pro Ile Asp Trp

33

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Leu Leu Asp His Ile Leu Trp Val Lys Val Cys Asn Pro Glu Lys
            335                     340                     345

Asp Ala Lys His Cys Asp Arg Gln Lys Ala Asn Leu Arg Ile Arg
            350                     355                     360

Phe Lys Pro Ser Leu Phe Gln His Val Gly Thr His Ser Ser Leu
            365                     370                     375

Ala Gly Lys Ile Gln Lys Leu Lys Asp Lys Asp Phe Gly Lys Gln
            380                     385                     390

Ala Leu Arg Lys Glu His Val Asn Pro Pro Ala Glu Val Ser Thr
            395                     400                     405

Ser Leu Lys Thr Tyr Gln His Phe Thr Leu Glu Lys Ala Tyr Leu
            410                     415                     420

Arg Glu Asp Phe Phe Trp Ala Phe Thr Pro Ala Ala Gly Asp Phe
            425                     430                     435

Ile Arg Phe Arg Phe Phe Gln Pro Leu Arg Leu Glu Arg Phe Phe
            440                     445                     450

Phe Arg Ser Gly Asn Ile Glu His Pro Glu Asp Lys Leu Phe Asn
            455                     460                     465

Thr Ser Val Glu Val Leu Pro Phe Asp Asn Pro Gln Ser Asp Lys
            470                     475                     480

Glu Ala Leu Gln Glu Gly Arg Thr Ala Thr Leu Arg Tyr Pro Arg
            485                     490                     495

Ser Pro Asp Gly Tyr Leu Gln Ile Gly Ser Phe Tyr Lys Gly Val
            500                     505                     510

Ala Glu Gly Glu Val Asp Pro Ala Phe Gly Pro Leu Glu Ala Leu
            515                     520                     525

Arg Leu Ser Ile Gln Thr Asp Ser Pro Val Trp Val Ile Leu Ser
            530                     535                     540

Glu Ile Phe Leu Lys Lys Ala Asp
            545
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<210> 25
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 25
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<210> 26
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 26
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<210> 27
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 27
 actcgggatt cctgctgtt 19

<210> 28
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 28
 aggcctttac ccaaggccac aac 23

<210> 29
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 29
 ggcctgtcct gtgttctca 19

<210> 30
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 30
 tcccaccact tacttccatg aa 22

<210> 31
<211> 25
<212> DNA
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<213> Artificial Sequence

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<223> Synthetic Oligonucleotide Probe

<400> 31
ctgtggtacc caattgccgc cttgt 25

<210> 32
<211> 23
<212> DNA
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<220>
<223> Synthetic Oligonucleotide Probe

<400> 32
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<210> 33
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 33
gtccagcaag ccctcatt 18

<210> 34
<211> 20
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<220>
<223> Synthetic Oligonucleotide Probe

<400> 34
cttctgggcc acagccctgc 20

<210> 35
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 35
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<210> 36
<211> 19
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 36
 ccagtcaggc cgttttaga 19

<210> 37
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 37
 cgggcgccca agtaaaagct c 21

<210> 38
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 38
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